Brain Segmentation using ATP (Automatic Twice PAM) in Multi Diffusion Indices

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Introduction

Volumetric measurements, spatial localizations, and shape descriptions of structures in the brain are adopted to understand the brain function and development [1]. Segmentation of neural architectures was studied and used widespreadly in the fundamental researches and applications. MRI provides the high quality of images and exceeding range of contrast, and thus it becomes an efficient modality for segmentation. Except T1-weighted, T2-weighted, and proton density-weighted images, diffusion tensor imaging (DTI) already becomes the modern technique for recognizing the constructions of brain. Tracking-based and orientation-based segment methods by DTI were attempted to describe the constituent components in this field [2-4]. However, prior spatial information or initializations in certain methods are necessary to be employed, which would directly affect the performance of results [5]. This study presents methods for brain structure segmentation by using automatic PAM (Partition Around Medoids) cluster method on various DTI indices with no prior information. PAM, one of the most widely used and practical methods for automatic clustering [6], was served as the kernel due to its robust ability with random initialization. 4 diffusion indices, fractional anisotropy (FA), relative anisotropy (RA), radial diffusivity (RD), and mean diffusivity (Trace{D}), derived from DTI were performed for clustering. Certain brain architectures can be automatically segmented and further evaluated by known anatomy.

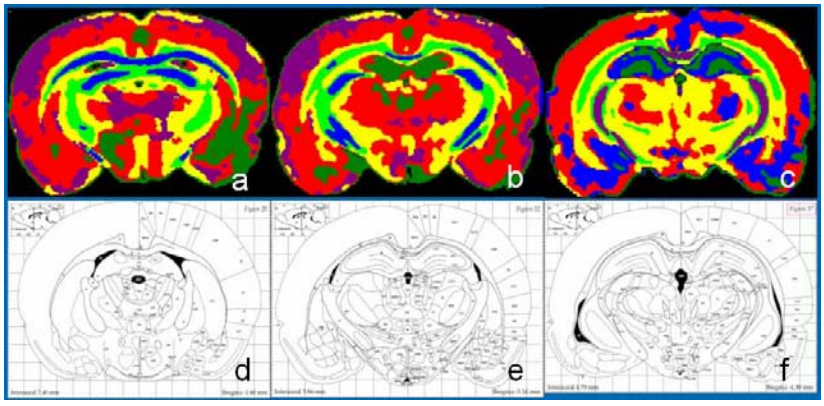
Materials and Methods

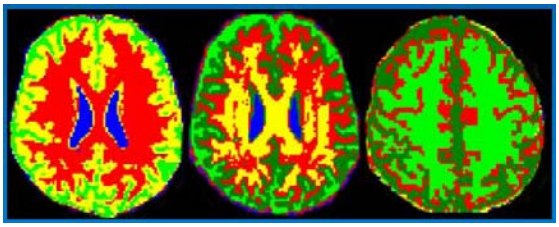
The rat brain was dissected from the cranium and was placed fixedly in an acrylic holder filled with 4% formaldehyde solution. The MR experiment was performed in a 9.4T MRI Biospec system (Bruker, Germany). DTI images were acquired using spin echo diffusion sequence with 257 diffusion-encoding directions within a 3D Cartesian lattice, matrix size =128×128, FOV = 20×20×1 mm^3, δ/Δ= 4.5/10 ms, TR/TE = 1500/18 ms, and b_{max} =14080 s mm^{-2}. All the procedures of animal experiment adhered to the guidelines for care and use of experimental animals of the lab animal center in National Yang-Ming University. Human brain images were acquired in a GE Healthcare Signa 1.5T Excite scanner by using spin echo EPI sequence with 252 diffusion-encoding directions, matrix size=128×128, slice number=4, voxel size=2.5×2.5×2.5 mm^3, TR/TE = 2000/91.2 ms and b_{max} =3000 s mm^{-2} . Diffusion indices, FA, RA, RD, and Trace{D}, were calculated according to the standard formula [7, 8].

PAM was selected to replace conventional k-means algorithm for the medoid is less influenced by noise or other extreme values. Twice cluster processes, with better processing speed, were implemented to segment the DTI data in this study. Regions of interesting were divided into several 16×16 square regions to proceed first clustering. The four features, FA, RA, Trace, and RD, were normalized to 0-1 for calculating the related distance between pixels. 12 cluster medoids in each divided region generated from the first clustering were grouped up to decide the final cluster medoids, from which all pixels would be re-assigned. The number of clusters in the second clustering step depended on that of structures in the ROI and the location of slices. No initial information or input prior to processing step is needed in our method. All programs were developed on our own by using Borland C++ Builder 6 and OpenGL API.

Results

The selected slice and clustered results are illustrated in Fig.1 and Fig.2. The second cluster numbers were assigned as 6 and 4 in the rat brain data and human brain data respectively. Brain structures such as corpus callosum (cc), cingulum (cg), internal capsule (ic), optic nerve (opt), dorsal 3rd ventricle (D3V), thalamus, and cerebral cortex were segmented using various color coding (fig. 1a-1c), which are well correlated with known anatomy (fig. 1d-1f). Figure 2 shows the segmentation results of human brain. White matter, gray matter, cerebral cortex, and ventricle can be clearly identified.





◀*Fig.1 The clustered results and the corresponding rat brain atlas. Brain architectures can be segmented by using our method.*

▲*Fig.2 Segmented results of human brain.*

Conclusions

Most prevalent techniques have recently made use of multi-modalities images to enhance information and the clustering algorithms to segment architectures automatically. Among those cluster algorithms, PAM is more robust than traditional k-means in the presence of noise but is more costly in signal processing. In this study, twice PAM was successfully implemented to improve this drawback. By incorporating diffusion characteristics from the multiple indices provides the potential to recognize brain architectures. Ultimately, the volumetric measurements and the detection of the distribution of each contrast would be applied by the recognition of specific brain regions.

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References

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